RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/574,045 _____
Source: _____ IFWP _____
Date Processed by STIC: _____ 04/07/2006 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 04/07/2006
PATENT APPLICATION: US/10/574,045   TIME: 11:02:40

Input Set : A:\14875-157US1.txt
Output Set: N:\CRF4\04072006\J574045.raw

```
 3 <110> APPLICANT: Matsushima, Kouji
 4        Hashimoto, Shinichi
 5        Tsuchiya, Masayuki
 6        Hirata, Yuichi
 7        Yoshida, Kenji
 8        Ojima, Kazuyuki
10 <120> TITLE OF INVENTION: PROTEIN EXPRESSED IN NK CELL
12 <130> FILE REFERENCE: 14875-157US1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/574,045
C--> 14 <141> CURRENT FILING DATE: 2005-03-28
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/14207
15 <151> PRIOR FILING DATE: 2004-09-29
17 <150> PRIOR APPLICATION NUMBER: JP 2003-338331
18 <151> PRIOR FILING DATE: 2003-09-29
20 <160> NUMBER OF SEQ ID NOS: 53
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1473
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (87)..(1376)
34 <400> SEQUENCE: 1
35 acacacccac aggacctgca gctgaacgaa gttgaagaca actcaggaga tctgttggaa      60
37 agagaacgat agaggaaaat atatga atg ttg cca tct tta gtt ccc tgt gtt     113
38                                 Met Leu Pro Ser Leu Val Pro Cys Val
39                                  1               5
41 ggg aaa act gtc tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt     161
42 Gly Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe
43 10                  15                  20                  25
45 gaa gga gat gcc ctg act ctg cga tgt cag gga tgg aag aat aca cca     209
46 Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro
47                 30                  35                  40
49 ctg tct cag gtg aag ttc tac aga gat gga aaa ttc ctt cat ttc tct     257
50 Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser
51                 45                  50                  55
53 aag gaa aac cag act ctg tcc atg gga gca gca aca gtg cag agc cgt     305
54 Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg
55         60                  65                  70
57 ggc cag tac agc tgc tct ggg cag gtg atg tat att cca cag aca ttc     353
58 Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe
59     75                  80                  85
```

```
 61 aca caa act tca gag act gcc atg gtt caa gtc caa gag ctg ttt cca       401
 62 Thr Gln Thr Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro
 63 90                  95                  100                 105
 65 cct cct gtg ctg agt gcc atc ccc tct cct gag ccc cga gag ggt agc       449
 66 Pro Pro Val Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser
 67                 110                 115                 120
 69 ctg gtg acc ctg aga tgt cag aca aag ctg cac ccc ctg agg tca gcc       497
 70 Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala
 71                 125                 130                 135
 73 ttg agg ctc ctt ttc tcc ttc cac aag gac ggc cac acc ttg cag gac       545
 74 Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp
 75             140                 145                 150
 77 agg ggc cct cac cca gaa ctc tgc atc ccg gga gcc aag gag gga gac       593
 78 Arg Gly Pro His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp
 79         155                 160                 165
 81 tct ggg ctt tac tgg tgt gag gtg gcc cct gag ggt ggc cag gtc cag       641
 82 Ser Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln
 83 170                 175                 180                 185
 85 aag cag agc ccc cag ctg gag gtc aga gtg cag gct cct gta tcc cgt       689
 86 Lys Gln Ser Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg
 87                 190                 195                 200
 89 cct gtg ctc act ctg cac cac ggg cct gct gac cct gct gtg ggg gac       737
 90 Pro Val Leu Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp
 91                 205                 210                 215
 93 atg gtg cag ctc ctc tgt gag gca cag agg ggc tcc cct ccg atc ctg       785
 94 Met Val Gln Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu
 95             220                 225                 230
 97 tat tcc ttc tac ctt gat gag aag att gtg ggg aac cac tca gct ccc       833
 98 Tyr Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro
 99         235                 240                 245
101 tgt ggt gga acc acc tcc ctc ctc ttc cca gtg aag tca gaa cag gat       881
102 Cys Gly Gly Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp
103 250                 255                 260                 265
105 gct ggg aac tac tcc tgc gag gct gag aac agt gtc tcc aga gag agg       929
106 Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg
107                 270                 275                 280
109 agt gag ccc aag aag ctg tct ctg aag ggt tct caa gtc ttg ttc act       977
110 Ser Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr
111                 285                 290                 295
113 ccc gcc agc aac tgg ctg gtt cct tgg ctt cct gcg agc ctg ctt ggc      1025
114 Pro Ala Ser Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly
115             300                 305                 310
117 ctg atg gtt att gct gct gca ctt ctg gtt tat gtg aga tcc tgg aga      1073
118 Leu Met Val Ile Ala Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg
119         315                 320                 325
121 aaa gct ggg ccc ctt cca tcc cag ata cca ccc aca gct cca ggt gga      1121
122 Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly
123 330                 335                 340                 345
125 gag cag tgc cca cta tat gcc aac gtg cat cac cag aaa ggg aaa gat      1169
```

RAW SEQUENCE LISTING   DATE: 04/07/2006
PATENT APPLICATION: US/10/574,045   TIME: 11:02:40

Input Set : **A:\14875-157US1.txt**
Output Set: **N:\CRF4\04072006\J574045.raw**

```
126 Glu Gln Cys Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp
127             350                 355             360
129 gaa ggt gtt gtc tac tct gtg gtg cat aga acc tca aag agg agt gaa        1217
130 Glu Gly Val Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu
131             365                 370             375
133 gcc agg tct gct gag ttc acc gtg ggg aga aag gac agt tct atc atc        1265
134 Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys Asp Ser Ser Ile Ile
135         380                 385             390
137 tgt gcg gag gtg aga tgc ctg cag ccc agt gag gtt tca tcc acg gag        1313
138 Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu Val Ser Ser Thr Glu
139     395                 400             405
141 gtg aat atg aga agc agg act ctc caa gaa ccc ctt agc gac tgt gag        1361
142 Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro Leu Ser Asp Cys Glu
143 410                 415             420             425
145 gag gtt ctc tgc tag tgatggtgtt ctcctatcaa cacacgccca cccccagtct        1416
146 Glu Val Leu Cys
149 ccagtgctcc tcaggaagac agtggggtcc tcaactcttt ctgtgggtcc ttcagtg       1473
152 <210> SEQ-ID NO: 2
153 <211> LENGTH: 429
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 2
158 Met Leu Pro Ser Leu Val Pro Cys Val Gly Lys Thr Val Trp Leu Tyr
159 1               5                 10              15
161 Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp Ala Leu Thr Leu
162             20                  25              30
164 Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val Lys Phe Tyr
165         35                  40              45
167 Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser
168     50                  55              60
170 Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly
171 65                  70              75                  80
173 Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala
174             85                  90                  95
176 Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile
177             100                 105             110
179 Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln
180         115                 120             125
183 Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe
184     130                 135             140
186 His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu
187 145                 150             155             160
189 Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu
190             165                 170             175
192 Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu
193             180                 185             190
195 Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His
196         195                 200             205
198 Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu
```

```
199     210                    215                   220
201 Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu
202 225                    230                   235                   240
204 Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu
205                    245                   250                   255
207 Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu
208                    260                   265                   270
210 Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser
211            275                   280                   285
213 Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val
214            290                   295                   300
216 Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala
217 305                    310                   315                   320
219 Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser
220                    325                   330                   335
222 Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala
223                    340                   345                   350
225 Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val
226         355                   360                   365
228 Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr
229     370                   375                   380
231 Val Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu
232 385                    390                   395                   400
234 Gln Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr
235                    405                   410                   415
237 Leu Gln Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys
238                    420                   425
241 <210> SEQ ID NO: 3
242 <211> LENGTH: 2005
243 <212> TYPE: DNA
244 <213> ORGANISM: Homo sapiens
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (88)..(1410)
251 <400> SEQUENCE: 3
252 cacacaccca caggacctgc agctgaacga agttgaagac aactcaggag atctgttgga      60
254 aagagaacga tagaggaaaa tatatga atg ttg cca tct tta ggc ccc atg ctg     114
255                                 Met Leu Pro Ser Leu Gly Pro Met Leu
256                                  1               5
258 ctc tgg acg gct gtg ctg ctc ttt gtt ccc tgt gtt ggg aaa act gtc     162
259 Leu Trp Thr Ala Val Leu Leu Phe Val Pro Cys Val Gly Lys Thr Val
260 10               15               20               25
262 tgg ctg tac ctc caa gcc tgg cca aac cct gtg ttt gaa gga gat gcc     210
263 Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp Ala
264             30                   35                   40
266 ctg act ctg cga tgt cag gga tgg aag aat aca cca ctg tct cag gtg     258
267 Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val
268             45                   50                   55
270 aag ttc tac aga gat gga aaa ttc ctt cat ttc tct aag gaa aac cag     306
```

```
271 Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln
272         60              65              70
274 act ctg tcc atg gga gca gca aca gtg cag agc cgt ggc cag tac agc    354
275 Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser
276         75              80              85
278 tgc tct ggg cag gtg atg tat att cca cag aca ttc aca caa act tca    402
279 Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser
280 90              95              100                 105
282 gag act gcc atg gtt caa gtc caa gag ctg ttt cca cct cct gtg ctg    450
283 Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu
284                 110             115             120
286 agt gcc atc ccc tct cct gag ccc cga gag ggt agc ctg gtg acc ctg    498
287 Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu
288                 125             130             135
290 aga tgt cag aca aag ctg cac ccc ctg agg tca gcc ttg agg ctc ctt    546
291 Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu
292             140             145             150
294 ttc tcc ttc cac aag gac ggc cac acc ttg cag gac agg ggc cct cac    594
295 Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His
296         155             160             165
298 cca gaa ctc tgc atc ccg gga gcc aag gag gga gac tct ggg ctt tac    642
299 Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr
300 170             175             180             185
302 tgg tgt gag gtg gcc cct gag ggt ggc cag gtc cag aag cag agc ccc    690
303 Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro
304                 190             195             200
306 cag ctg gag gtc aga gtg cag gct cct gta tcc cgt cct gtg ctc act    738
307 Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr
308                 205             210             215
310 ctg cac cac ggg cct gct gac ccc gct gtg ggg gac atg gtg cag ctc    786
311 Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu
312             220             225             230
314 ctc tgt gag gca cag agg ggc tcc cct ccg atc ctg tat tcc ttc tac    834
315 Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr
316         235             240             245
318 ctt gat gag aag att gtg ggg aac cac tca gct ccc tgt ggt gga acc    882
319 Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr
320 250             255             260             265
322 acc tcc ctc ctc ttc cca gtg aag tca gaa cag gat gct ggg aac tac    930
323 Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr
324             270             275             280
326 tcc tgc gag gct gag aac agt gtc tcc aga gag agg agt gag ccc aag    978
327 Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys
328             285             290             295
330 aag ctg tct ctg aag ggt tct caa gtc ttg ttc act ccc gcc agc aac    1026
331 Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn
332             300             305             310
334 tgg ctg gtt cct tgg ctt cct gcg agc ctg ctt ggc ctg atg gtt att    1074
335 Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/07/2006
PATENT APPLICATION: US/10/574,045   TIME: 11:02:41

Input Set : A:\14875-157US1.txt
Output Set: N:\CRF4\04072006\J574045.raw

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31
Seq#:32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53

VERIFICATION SUMMARY   DATE: 04/07/2006
PATENT APPLICATION: US/10/574,045   TIME: 11:02:41

Input Set : **A:\14875-157US1.txt**
Output Set: **N:\CRF4\04072006\J574045.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date